

Nancy Johnson

#6

PAGE: 1

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/162,597**

DATE: 01/06/99  
TIME: 20:33:28

### **INPUT SET: S30604.raw**

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

1 SEQUENCE LISTING

### 3 (1) General Information

5 (i) APPLICANT: Bandman, Olga  
6 Au-Young, Janice  
7 Goli, Surya K.  
8 Hillman, Jennifer.  
9 Zweiger, Gary B.

10  
11 (ii) TITLE OF THE INVENTION: A NOVEL TUMOR PROTEIN

13 (iii) NUMBER OF SEQUENCES: 7

15 (iv) CORRESPONDENCE ADDRESS:  
16 (A) ADDRESSEE: Incyte Phar  
17 (B) STREET: 3174 Porter Dr  
18 (C) CITY: Palo Alto  
19 (D) STATE: CA  
20 (E) COUNTRY: U.S.  
21 (F) ZIP: 94304

23 (v) COMPUTER READABLE FORM:  
24 (A) MEDIUM TYPE: Diskette  
25 (B) COMPUTER: IBM Compatible  
26 (C) OPERATING SYSTEM: DOS  
27 (D) SOFTWARE: FastSEQ Version 1.5

29 (vi) CURRENT APPLICATION DATA:  
30 (A) APPLICATION NUMBER: 09/162,597  
31 (B) FILING DATE:

32  
33 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: 08/715,204  
35 (B) FILING DATE:

42 (ix) TELECOMMUNICATION INFORMATION:  
43 (A) TELEPHONE: 415-855-0555  
44 (B) TELEFAX: 415-845-4166

46 (2) INFORMATION FOR SEQ ID NO:1:

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/162,597**DATE: 01/06/99  
TIME: 20:33:29**INPUT SET: S30604.raw**

47  
48       (i) SEQUENCE CHARACTERISTICS:  
49           (A) LENGTH: 204 amino acids  
50           (B) TYPE: amino acid  
51           (C) STRANDEDNESS: single  
52           (D) TOPOLOGY: linear  
53  
54       (ii) MOLECULE TYPE: peptide  
55       (vii) IMMEDIATE SOURCE:  
56           (A) LIBRARY:  
57           (B) CLONE: Consensus  
58  
59       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
60  
61       Met Glu Ala Gln Ala Gln Gly Leu Leu Glu Thr Glu Pro Leu Gln Gly  
62        1                   5                   10                   15  
63       Thr Asp Glu Asp Ala Val Ala Ser Ala Asp Phe Ser Ser Met Leu Ser  
64        20                  25                   30  
65       Glu Glu Glu Lys Glu Glu Leu Lys Ala Glu Leu Val Gln Leu Glu Asp  
66        35                  40                   45  
67       Glu Ile Thr Thr Leu Arg Gln Val Leu Ser Ala Lys Glu Arg His Leu  
68        50                  55                   60  
69       Val Glu Ile Lys Gln Lys Leu Gly Met Asn Leu Met Asn Glu Leu Lys  
70        65                  70                   75                   80  
71       Gln Asn Phe Ser Lys Ser Trp His Asp Met Gln Thr Thr Ala Tyr  
72        85                  90                   95  
73       Lys Lys Thr His Glu Thr Leu Ser His Ala Gly Gln Lys Ala Thr Ala  
74        100                105                   110  
75       Ala Phe Ser Asn Val Gly Thr Ala Ile Ser Lys Lys Phe Gly Asp Met  
76        115                120                   125  
77       Ser Tyr Ser Ile Arg His Ser Ile Ser Met Pro Ala Met Arg Asn Ser  
78        130                135                   140  
79       Pro Thr Phe Lys Ser Phe Glu Glu Arg Val Glu Thr Thr Val Thr Ser  
80        145                150                   155                   160  
81       Leu Lys Thr Lys Val Gly Gly Thr Asn Pro Asn Gly Gly Ser Phe Glu  
82        165                170                   175  
83       Glu Val Leu Ser Ser Thr Ala His Ala Ser Ala Gln Ser Leu Ala Gly  
84        180                185                   190  
85       Gly Ser Arg Arg Thr Lys Glu Glu Leu Gln Cys  
86        195                200

87  
88       (2) INFORMATION FOR SEQ ID NO:2:  
89

90       (i) SEQUENCE CHARACTERISTICS:  
91           (A) LENGTH: 790 base pairs  
92           (B) TYPE: nucleic acid  
93           (C) STRANDEDNESS: single  
94           (D) TOPOLOGY: linear  
95  
96       (ii) MOLECULE TYPE: cDNA  
97  
98       (vii) IMMEDIATE SOURCE:  
99           (A) LIBRARY:



**RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/162,597**

DATE: 01/06/99  
TIME: 20:33:31

**INPUT SET: S30604.raw**

153	His Tyr Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp			
154	145	150	155	160
155	Leu Tyr His Asn Phe Arg Pro Ala Val Leu Leu Leu Met Phe Leu Ser			
156	165	170	175	
157	Val Tyr Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu			
158	180	185	190	
159	Gly Ser Trp Ala Arg Leu Asp Ala Arg Ala Val Val Thr Gly Leu Leu			
160	195	200	205	
161	Ala Leu Lys His Phe Gly Pro Val Cys Arg Arg Cys Gln Cys Ala Leu			
162	210	215	220	
163	Leu Gly Leu Val Ser Gln Thr Leu Met Tyr Leu Phe Pro Ala Ser Leu			
164	225	230	235	240
165	Gln Val Leu Val Lys			
166	245			

167

(2) INFORMATION FOR SEQ ID NO:4:

168

(i) SEQUENCE CHARACTERISTICS:

169

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

170

(ii) MOLECULE TYPE: cDNA

171

(vii) IMMEDIATE SOURCE:

172

(A) LIBRARY:

173

(B) CLONE: Consensus

174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

175

184	GTGMGMKCGCG GGCCCCCGCC AGTCAGGTGG GTGCCAGGCC CTGGCCGTGG CGAAAGAGCC	60
185	GGCGGAGGGA GGACCCGCTC CCGGAGACGC CGCCTCGCGA TCCCCGCGCG GGCAGGGACCG	120
186	GGCGGCCGGC ATCATGACCC TGTTCACTT CGGAACTGC TTGCGCTTTG CCTACTTCCC	180
187	CTACTTCATC ACCTACAAGT GCAGCGGCCT GTCCGAGTAC AACGCCTTCT GGAAATGCGT	240
188	CCAGGCTGGA GTCACCTACC TCTTGTCGA ACTCTGCAAG ATGCTGTTCT TGGCCACTTT	300
189	CTTTCCCACC TGGGAAGGCG GCATCTATGA CTTCATTGGG GAGTTCATGA AGGCCAGCGT	360
190	GGATGTGGCA GACCTGATAG GTCTAACCT TGTCATGTCC CGGAATGCCG GCAAGGGAGA	420
191	GTACAAGATC ATGGTTGCTG CCCCTGGGCTG GGCCACTGCT GAGCTTATTA TGTCCCGCTG	480
192	CATTCCCCTA TGGGTGGAG CCCGGGGCAT TGAGTTGAC TGGAAGTACA TCCAGATGAG	540
193	CATAGACTCC AACATCAGTC TGGTCCATT CATCGTCGCG TCTGCTCAGG TCTGGATGAT	600
194	AACACGCTAT GATCTGTACC ACAACTTCCG GCCAGCTGTC CTTCTGCTGA TGTTCCCTCAG	660
195	TGTCTACAAG GCCTTTGTTA TGGAGACCTT CGTCCACCTC TGCTCGCTGG GCAGTTGGGC	720
196	ARCTCTAMTG GCCCCGAGCAG TGGTAACGGG GCTGCTGGCC CTCAAGCACT TTGGSCCTGT	780
197	ATGTCGSCGT TGTCAATGTG CACTYCTAGG CTTGGTGTCT CAGACATTGA TGTACCTTT	840
198	CCCTGCCTCA CTCCAGGTTT TAGTGAAGTA AACAGTATTT GGAAAGTT	888

199

(2) INFORMATION FOR SEQ ID NO:5:

200

(i) SEQUENCE CHARACTERISTICS:

201

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

202

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/162,597DATE: 01/06/99  
TIME: 20:33:31

INPUT SET: S30604.raw

206                   (D) TOPOLOGY: linear  
207  
208                   (ii) MOLECULE TYPE: peptide  
209  
210                   (vii) IMMEDIATE SOURCE:  
211                    (A) LIBRARY: GenBank  
212                    (B) CLONE: 790225  
213  
214                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
215  
216       Met Asp Arg Gly Glu Gln Gly Leu Leu Arg Thr Asp Pro Val Pro Glu  
217        1               5               10               15  
218       Glu Gly Glu Asp Val Ala Ala Thr Ile Ser Ala Thr Glu Thr Leu Ser  
219        20              25               30  
220       Glu Glu Glu Gln Glu Glu Leu Arg Arg Glu Leu Ala Lys Val Glu Glu  
221        35              40               45  
222       Glu Ile Gln Thr Leu Ser Gln Val Leu Ala Ala Lys Glu Lys His Leu  
223        50              55               60  
224       Ala Glu Ile Lys Arg Lys Leu Gly Ile Asn Ser Leu Gln Glu Leu Lys  
225        65              70               75               80  
226       Gln Asn Ile Ala Lys Gly Trp Gln Asp Val Thr Ala Thr Ser Ala Tyr  
227        85              90               95  
228       Lys Lys Thr Ser Glu Thr Leu Ser Gln Ala Gly Gln Lys Ala Ser Ala  
229        100             105              110  
230       Ala Phe Ser Ser Val Gly Ser Val Ile Thr Lys Lys Leu Glu Asp Val  
231        115             120              125  
232       Lys Asn Ser Pro Thr Phe Lys Ser Phe Glu Glu Lys Val Glu Asn Leu  
233        130             135              140  
234       Lys Ser Lys Val Gly Gly Thr Lys Pro Ala Gly Gly Asp Phe Gly Glu  
235        145             150              155              160  
236       Val Leu Asn Ser Ala Ala Asn Ala Ser Ala Thr Thr Thr Glu Pro Leu  
237        165             170              175  
238       Pro Glu Lys Thr Gln Glu Ser Leu  
239        180  
240  
241                   (2) INFORMATION FOR SEQ ID NO:6:  
242  
243                   (i) SEQUENCE CHARACTERISTICS:  
244                    (A) LENGTH: 257 amino acids  
245                    (B) TYPE: amino acid  
246                    (C) STRANDEDNESS: single  
247                    (D) TOPOLOGY: linear  
248  
249                   (ii) MOLECULE TYPE: peptide  
250  
251                   (vii) IMMEDIATE SOURCE:  
252                    (A) LIBRARY: GenBank  
253                    (B) CLONE: 1072344  
254  
255                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
256  
257       Met Pro Lys Gly Asn Lys Lys Pro Asn Glu Lys Lys Glu Glu Leu Glu  
258        1               5               10               15

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION **US/09/162,597**

DATE: 01/06/99  
TIME: 20:33:32

***INPUT SET: S30604.raw***

Line

Error

Original Text